OIPE

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/10/088,045   TIME: 16:23:41

        Input Set : N:\Crf3\04042002\J088045.raw
        Output Set: N:\CRF3\04092002\J088045.raw

 1 <110> APPLICANT: Joelle Thonnard
 2 <120> TITLE OF INVENTION: Novel Compounds
 3 <130> FILE REFERENCE: BM45412
 4 <140> CURRENT APPLICATION NUMBER: US/10/088,045
 5 <141> CURRENT FILING DATE: 2002-03-14
 6 <150> PRIOR APPLICATION NUMBER: 9921691.3
 7 <151> PRIOR FILING DATE: 1999-09-14
 8 <160> NUMBER OF SEQ ID NOS: 10
 9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1509
13 <212> TYPE: DNA
14 <213> ORGANISM: Moraxella catarrhalis
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17   agtggttgta gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggtagacgct   120
18   gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct   180
19   gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac   240
20   cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc   300
21   gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt   360
22   gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat   420
23   gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg   480
24   ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt   540
25   gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa   600
26   ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat   660
27   accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga   720
28   gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct   780
29   ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg   840
30   acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag   900
31   ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa   960
32   tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt   1020
33   aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca   1080
34   cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa   1140
35   gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca   1200
36   acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct   1260
37   ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc   1320
38   gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg   1380
39   cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc   1440
40   tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaaagccaa aaaaaccaag   1500
41   ccaaactga   1509
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 502
45 <212> TYPE: PRT

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46 <213> ORGANISM: Moraxella catarrhalis
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50      Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
51                   20                  25                  30
52      Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
53                   35                  40                  45
54      Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
55           50                  55                  60
56      Ile Val Thr His Ala Pro Glu Val Pro Pro Val Asp Arg Asp His
57      65                  70                  75                  80
58      Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
59                       85                  90                  95
60      Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
61                   100                 105                 110
62      Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
63                   115                 120                 125
64      Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
65           130                 135                 140
66      Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
67      145                 150                 155                 160
68      Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
69                       165                 170                 175
70      Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
71                   180                 185                 190
72      Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
73                   195                 200                 205
74      Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
75           210                 215                 220
76      Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
77      225                 230                 235                 240
78      Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
79                   245                 250                 255
80      Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
81                   260                 265                 270
82      Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
83                   275                 280                 285
84      Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
85           290                 295                 300
86      Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
87      305                 310                 315                 320
88      Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
89                   325                 330                 335
90      Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
91                   340                 345                 350
92      Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
93                   355                 360                 365
94      Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
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 95            370                  375                  380
 96      Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
 97      385                  390                  395                  400
 98      Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
 99              .         405                  410                  415
100          Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
101                      420                  425                  430
102          Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
103              435                  440                  445
104          Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
105              450             .        455                  460
106          Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
107          465                  470         .        475                  480
108          Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
109                      485                  490                  495
110          Lys Lys Thr Lys Pro Asn
111                      500
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 1506
115 <212> TYPE: DNA
116 <213> ORGANISM: Moraxella catarrhalis
117 <400> SEQUENCE: 3
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119      agtggttgta gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggtagacgct      120
120      gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct      180
121      gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac      240
122      cccgccaaag tggtggtaaa aatggaaacc gttgaaaaag tcatgcgtct ggcagatggc      300
123      gtggaatatc agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt      360
124      gaaggcgaca ccatcgaagt gcagttctca aaccacccag attcaaaaat gccccataat      420
125      gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg      480
126      ggtcatacat caacctttag tttaaagcc ttacagcctg gtttgtatgt ctatcactgt      540
127      gcggttgccc ctgttggcat gcacattgct aatggcatgt atggtttgat tttggttgaa      600
128      ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgactttat       660
129      accaaaggca aatatggcga acaaggtcta cagcccttg atatggaaaa agccattcga       720
130      gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct      780
131      ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg      840
132      acatcatcat ccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtaag      900
133      ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa      960
134      tttaaggtgg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt     1020
135      aacaaagggg cattgggcat acttaaggtg gaaggtgaag aaaatcatga gatttattca     1080
136      cacaaacaaa cagacgctgt ctatctgcca gagggtgccc cacaagcaat tgatacccaa     1140
137      gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca     1200
138      acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct     1260
139      ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc     1320
140      gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg     1380
141      cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc     1440
142      tttggtaaca aaggcggtca actcagtgca gacgatgtgg caaagccaa aaaaccaag      1500
143      ccaaac                                                               1506
145 <210> SEQ ID NO: 4
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146 <211> LENGTH: 502
147 <212> TYPE: PRT
148 <213> ORGANISM: Moraxella catarrhalis
149 <400> SEQUENCE: 4
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153                 20                  25                  30
154     Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
155             35                  40                  45
156     Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
157         50                  55                  60
158     Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
159     65                  70                  75                  80
160     Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
161                 85                  90                  95
162     Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
163                 100                 105                 110
164     Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
165             115                 120                 125
166     Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
167         130                 135                 140
168     Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
169     145                 150                 155                 160
170     Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
171                 165                 170                 175
172     Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
173                 180                 185                 190
174     Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
175                 195                 200                 205
176     Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
177         210                 215                 220
178     Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
179     225                 230                 235                 240
180     Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
181                 245                 250                 255
182     Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
183                 260                 265                 270
184     Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
185                 275                 280                 285
186     Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
187         290                 295                 300
188     Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
189     305                 310                 315                 320
190     Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
191                 325                 330                 335
192     Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
193             340                 345                 350
194     Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
```

```
195            355                360                365
196      Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
197          370                375                380
198      Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
199      385                390                395                400
200      Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
201              405                410                415
202      Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
203              420                425                430
204      Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
205          435                440                445
206      Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
207          450                455                460
208      Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
209      465                470                475                480
210      Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
211              485                490                495
212      Lys Lys Thr Lys Pro Asn
213              500
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 21
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: primer
221 <400> SEQUENCE: 5
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225 <211> LENGTH: 23
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: primer
230 <400> SEQUENCE: 6
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234 <211> LENGTH: 17
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: primer
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240      gtaaaacgac ggccagt                                               17
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243 <211> LENGTH: 17
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: primer
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VERIFICATION SUMMARY   DATE: 04/09/2002
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